

BASE COUNT 78 a 31 c 36 g 99 t
 ORIGIN

Query Match 4.7%; Score 19; DB 59; Length 244;
 Best Local Similarity 100.0%; Pred. No. 12;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 CCTCATATTTTCAGAAAT 28

RESULT 2
 AA650451/c 359 bp MRNA EST 13-NOV-1997
 LOCUS ns98a11.s1 NCI-CGAP-Br4 Homo sapiens CDNA clone IMAGE:1191644
 DEFINITION similar to contains Alu repetitive element; mRNA sequence.
 ACCESSION AA650451 GI:2577779
 VERSION AA650451.1 GI:2577779
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 359)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/cgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 TITLE Unpublished (1997)

JOURNAL On Jan 19, 1998 this sequence version replaced GI:2286482.
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1350
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Ian Kirsch, M.D., Kristina A. Cole, M.D.,
 P.D. student, Rodrigo F. Chuquil, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.
 CDNA Library Preparation: David B. Kitzman, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www-bio.lnl.gov/dbp/image/image.html
 Insert Length: 444 Std Error: 0.00
 Seq primer: -40ml3 fwd. RT from Amersham.

FEATURES

source

1. 359
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1191644"
 /clone_lib="NCI-CGAP-Br4"
 /sex="female"
 /tissue_type="normal ductal tissue"
 /lab_host="DH10B"
 /note="Organ: breast; Vector: PAMP10; mRNA made from
 normal breast ductal tissue, cDNA made by oligo-dT
 priming. Non-directionally cloned. Size selected on
 agarose gel, average insert size 600 bp. Reference:
 Kitzman et al. (1996) Cancer Research 56:5380-5381."
 BASE COUNT 63 a 88 c 77 g 131 t
 ORIGIN

Query Match 4.7%; Score 19; DB 29; Length 359;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 aaaccacagtaggaataa 117
 244 aaaccacagtaggaataa 226

RESULT 3
 AQ100432 377 bp DNA GSS 27-AUG-1998
 LOCUS HS.3055-41.F05 MF CIR Approved Human Genomic Sperm Library D
 DEFINITION Homo sapiens genomic clone Plate-3055 Col-9 Row-K, genomic
 survey sequence.
 ACCESSION AQ100432

VERSION AQ100432.1 GI:3471461
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 377)
 Mahalras G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,
 Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
 Hood L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U. S. A. 96 (17): 9739-9744 (1999)
 JOURNAL 99380589
 MEDLINE
 COMMENT Contact: Mahalras G.G., Wallace J.C., Hood L.
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3055 Row: K Column: 9
 Class: BAC ends
 High quality sequence stop: 377.

FEATURES

source

1. 377
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_plate="3055 Col-9 Row-K"
 /clone_lib="CIR Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
 E-Coli DH10B"
 BASE COUNT 82 a 108 c 101 g 81 t 5 others
 ORIGIN

Query Match 4.7%; Score 19; DB 94; Length 377;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 36 ttacgctctctgtgttc 54
 9 ttacgctctctgtgttc 27

RESULT 4
 AQ352552 470 bp DNA GSS 24-JAN-1999
 LOCUS CTBR-EL-254101.TF CIRBr-El Homo sapiens genomic clone 254101,
 DEFINITION genomic survey sequence.
 ACCESSION AQ352552

VERSION AQ352552.1 GI:4179887
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 470)
 Zhao S., Adams M.D., Nierman W., Malek J., Shizuya H., Simon M. and
 Venter J.C.
 Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building

Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ttctataataaaattgtgaa 306
 Db 286 ttctataataaaattgtgaa 48

RESULT 10
 SOYMOD26A 5831 bp DNA PLN 14-OCT-1993
 DEFINITION Glycine max cv. Dare nodulin 26 gene fragment.
 ACCESSION M94764
 VERSION M94764.1 GI:170029
 KEYWORDS
 SOURCE Glycine max (cultivar Dare) DNA.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.

REFERENCE 1 (bases 1 to 5831)
 AUTHORS Miao, G.H. and Verma, D.P.
 TITLE Soybean nodulin-26 gene encoding a channel protein is expressed only in the infected cells of nodules and is regulated differently in roots of homologous and heterologous plants
 JOURNAL Plant Cell 5 (7), 781-794 (1993)
 MEDLINE 93372569
 FEATURES
 source location/Qualifiers
 1..5831
 /organism="Glycine max"
 /db_xref="taxon:3847"

BASE COUNT 2029 a 824 c 877 g 2101 t
 ORIGIN

Query Match 6.8%; Score 21; DB 7; Length 5831;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 acctgcaagctttgtgttg 101
 Db 2648 ACCTGCAAGCTTTGTGTG 2668

RESULT 11
 AC025334/C 71804 bp DNA HTG 08-MAR-2000
 LOCUS Homo sapiens chromosome 2 clone RP11-358M3 map 2, LOW-PASS SEQUENCE
 DEFINITION
 SAMPLING.
 ACCESSION AC025334
 VERSION AC025334
 KEYWORDS HTG; HTGS-PHASE0.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 71801)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Homo sapiens chromosome 2, clone RP11-358M3
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 71801)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, B., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, E., Boguski, L., Boucknight, B., Brown, A., Burkett, C., Campilongo, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardina, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hages, B., Heathford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klei, J., Laroque, K., Lamazares, R., Landes, T., Lenock, J., Levine, R., Liu, G., Liu, K., Locke, K., MacDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R.,

TITLE JOURNAL COMMENT

Meldrum, J., Meneus, L., Mithova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, G.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisanil, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 ALL repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: MIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence-submissions@genome.wi.mit.edu
 Project Information
 Center project name: L6454
 Center clone name: 358_M3

NOTE: This record contains 84 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1
 747 846: contig of 746 bp in length
 847 1601: contig of 755 bp in length
 1602 1701: gap of 100 bp
 1702 2462: contig of 761 bp in length
 2463 2562: gap of 100 bp
 2563 3321: contig of 759 bp in length
 3322 3421: gap of 100 bp
 3422 4158: contig of 737 bp in length
 4159 4258: gap of 100 bp
 4259 5011: contig of 753 bp in length
 5012 5111: gap of 100 bp
 5112 5874: contig of 763 bp in length
 5875 5974: gap of 100 bp
 5975 6704: contig of 730 bp in length
 6705 6804: gap of 100 bp
 6805 7562: contig of 758 bp in length
 7563 7662: gap of 100 bp
 7663 8434: contig of 772 bp in length
 8435 8534: gap of 100 bp
 8535 9298: contig of 764 bp in length
 9299 9398: gap of 100 bp
 9399 10157: contig of 759 bp in length
 10158 10257: gap of 100 bp
 10258 10999: contig of 742 bp in length
 11000 11099: gap of 100 bp
 11100 11854: contig of 755 bp in length
 11855 11954: gap of 100 bp
 11955 12717: contig of 763 bp in length
 12718 12817: gap of 100 bp
 12818 13568: contig of 751 bp in length
 13569 13668: gap of 100 bp
 13669 14423: contig of 755 bp in length
 14424 14523: gap of 100 bp
 14524 15288: contig of 765 bp in length
 15289 15388: gap of 100 bp
 15389 16435: contig of 747 bp in length
 16136 16235: gap of 100 bp

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 72 | 16.2 | 162 | 27 | AA493099 |
| 2 | 55 | 12.4 | 300 | 90 | W07101 |
| 3 | 55 | 12.4 | 451 | 39 | AA417464 |
| 4 | 55 | 12.4 | 496 | 32 | AA857673 |
| 5 | 55 | 12.4 | 497 | 71 | AA328446 |
| 6 | 55 | 12.4 | 498 | 37 | AI277373 |
| 7 | 55 | 12.4 | 504 | 39 | AI439816 |
| 8 | 55 | 12.4 | 513 | 37 | AI278440 |
| 9 | 55 | 12.4 | 525 | 27 | AA435639 |
| 10 | 55 | 12.4 | 534 | 29 | AA490602 |
| 11 | 55 | 12.4 | 551 | 27 | AA480162 |
| 12 | 55 | 12.4 | 554 | 29 | AA663472 |
| 13 | 55 | 12.4 | 554 | 29 | AA663472 |
| 14 | 55 | 11.5 | 308 | 102 | AA439530 |
| 15 | 51 | 11.5 | 420 | 47 | AI983716 |
| 16 | 51 | 11.5 | 420 | 38 | AI332615 |
| 17 | 51 | 11.5 | 457 | 79 | AA674023 |
| 18 | 50 | 11.2 | 572 | 63 | AA103030 |
| 19 | 50 | 11.2 | 556 | 73 | AA499920 |
| 20 | 47 | 10.6 | 354 | 107 | AA323354 |
| 21 | 47 | 10.6 | 454 | 98 | AA180060 |
| 22 | 47 | 10.6 | 523 | 96 | AA277318 |
| 23 | 47 | 10.6 | 526 | 111 | AA692714 |
| 24 | 46 | 10.3 | 544 | 43 | AI744949 |
| 25 | 45 | 10.1 | 485 | 95 | AA167057 |
| 26 | 45 | 10.1 | 489 | 110 | AA799581 |
| 27 | 45 | 10.1 | 622 | 120 | BA48282 |
| 28 | 45 | 10.1 | 864 | 101 | AA342901 |
| 29 | 44 | 9.9 | 186 | 28 | AA576792 |
| 30 | 44 | 9.9 | 344 | 70 | AA302950 |
| 31 | 44 | 9.9 | 375 | 35 | AI144036 |
| 32 | 44 | 9.9 | 420 | 21 | AA085410 |
| 33 | 43 | 9.7 | 353 | 27 | AA507837 |
| 34 | 43 | 9.7 | 667 | 22 | AA196790 |
| 35 | 43 | 9.7 | 990 | 110 | AA747348 |
| 36 | 42 | 9.4 | 627 | 27 | AA490097 |
| 37 | 42 | 9.4 | 627 | 94 | AA114141 |
| 38 | 42 | 9.4 | 629 | 107 | AA635928 |
| 39 | 42 | 9.4 | 629 | 107 | AA635928 |
| 40 | 41 | 9.2 | 425 | 21 | AA847029 |
| 41 | 41 | 9.2 | 454 | 105 | AA475892 |
| 42 | 40 | 9.0 | 299 | 96 | AA316521 |
| 43 | 40 | 9.0 | 374 | 94 | AA103431 |
| 44 | 40 | 9.0 | 403 | 31 | AA831408 |
| 45 | 40 | 9.0 | 417 | 27 | AA487412 |

ALIGNMENTS

RESULT 1
LOCUS AA493099/c
DEFINITION 162 bp mRNA
EST 19-AUG-1997
n996d01.s1 NCI-CCAP_Thy1 Homo sapiens cDNA clone IMAGE:942625
Similar to contains Alu repetitive element; contains element M99

NCBI repetitive element ;, mRNA sequence.
AA493099
VERSION AA493099.1 GI:2222940
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 14, 1998 this sequence version replaced gi:1798572.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdrrp/image/image.html
Insert length: 451 Std Error: 0.00
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 153.
Location/Qualifiers
1. 162
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:942625"
/clone_lib="NCI-CCAP_Thy1"
/tissue_type="thyroid"
/lab_host="DH10B"
/note="Vector: pAMP10; mRNA made from invasive thyroid tumor, CDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 47 a 36 c 50 g 29 t
ORIGIN
Query Match 16.2%; Score 72; DB 27; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.3e-24;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 275 tttagacagcgggttcgcacacctgcagcagctgtctgaactcctgacctgtg 334
DB 162 tttagacagcgggttcgcacacctgcacacctgtctgaactcctgacctgtg 103
OY 335 atctaccacct 346
DB 102 atctaccacct 91
RESULT 2
LOCUS W07101/c
DEFINITION 300 bp mRNA
EST 25-APR-1996
IMAGE:300107.5, similar to contains Alu repetitive element; contains element M922 repetitive element ;, mRNA sequence.
ACCESSION W07101
VERSION W07101.1 GI:1281414
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Hillier, L., Clark, N., Dubuque, J., Elliston, K., Hawkins, M.,

| | | | |
|------|-------------|-----------|---|
| 117: | gb_gss913:* | | MERF repetitive element ; , mRNA sequence. |
| 118: | gb_gss914:* | ACCESSION | AA493099 |
| 119: | gb_gss915:* | VERSION | AA493099.1 |
| 120: | gb_gss916:* | KEYWORDS | GT:2222940 |
| 121: | gb_gss917:* | SOURCE | EST. |
| 122: | gb_gss918:* | ORGANISM | human. |
| 123: | gb_gss919:* | | Homo sapiens |
| 124: | em_gss913:* | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 to 153) |

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|-------|----------------|--------|----|----|-------------|
|---------------|-------|----------------|--------|----|----|-------------|

| | | | | | | | | |
|---|----|-----|------|-----|-----|-----------|-----------|-------------|
| C | 1 | 119 | 24.5 | 162 | 27 | AA493099 | AA493099 | ng96d01.s |
| C | 2 | 55 | 11.3 | 300 | 90 | W07101 | W07101 | z493d06.r1 |
| C | 3 | 55 | 11.3 | 451 | 39 | AI147464 | AI147464 | tlh3h02.x |
| C | 4 | 55 | 11.3 | 496 | 32 | AA857673 | AA857673 | oe41fc05.s |
| C | 5 | 55 | 11.3 | 497 | 71 | AM328446 | AM328446 | ds02fc03.y |
| C | 6 | 85 | 11.3 | 498 | 37 | AI2777373 | AI2777373 | qms4c07.x |
| C | 7 | 55 | 11.3 | 504 | 39 | AI439816 | AI439816 | tl36d10.x |
| C | 8 | 55 | 11.3 | 513 | 37 | AI278440 | AI278440 | qms3c11.x |
| C | 9 | 55 | 11.3 | 525 | 39 | AI435659 | AI435659 | tlh47h01.x |
| C | 10 | 55 | 11.3 | 534 | 27 | AA490602 | AA490602 | aa47f08.s |
| C | 11 | 55 | 11.3 | 551 | 27 | AA460152 | AA480162 | ne30b07.s |
| C | 12 | 55 | 11.3 | 954 | 27 | AA663472 | AA654472 | pc51e05.s |
| C | 13 | 55 | 10.5 | 308 | 102 | AA0399330 | AA039930 | HS_5091 |
| C | 14 | 51 | 10.5 | 420 | 47 | AI963716 | AI963716 | w23c11.x |
| C | 15 | 51 | 10.5 | 520 | 38 | AI9332615 | AI9332615 | qps4d11.x |
| C | 16 | 51 | 10.5 | 572 | 79 | AM674403 | AM674403 | ba59y11.x |
| C | 17 | 50 | 10.3 | 354 | 101 | AA0354250 | AA034250 | CITBI-E1 |
| C | 18 | 50 | 10.3 | 455 | 63 | AM103030 | AM103030 | x442c09.x |
| C | 19 | 50 | 10.3 | 556 | 73 | AA499920 | AA499920 | UI-HF-BNO |
| C | 20 | 48 | 9.9 | 245 | 96 | AQ322354 | AQ322354 | RPC111-10 |
| C | 21 | 47 | 9.7 | 454 | 95 | AO180060 | AO180060 | HS_3204-B |
| C | 22 | 47 | 9.7 | 523 | 96 | AQ277318 | AQ277318 | CITBI-E1 |
| C | 23 | 47 | 9.7 | 526 | 111 | AA0927114 | AA0927114 | HS_3415 |
| C | 24 | 47 | 9.7 | 541 | 43 | AI744949 | AI744949 | tlr17f04.x |
| C | 25 | 45 | 9.3 | 485 | 110 | AO799581 | AO799581 | HS_3151-B |
| C | 26 | 45 | 9.3 | 489 | 95 | AA167057 | AA167057 | HS_4507-B |
| C | 27 | 45 | 9.3 | 622 | 120 | B48282 | B48282 | RPC111-6m8 |
| C | 28 | 45 | 9.3 | 864 | 101 | AQ342801 | AQ342801 | RPC111-121 |
| C | 29 | 44 | 9.1 | 186 | 28 | AA576792 | AA576792 | nm7b08.s |
| C | 30 | 44 | 9.1 | 344 | 70 | AM302980 | AM302980 | x158d12.x |
| C | 31 | 44 | 9.1 | 375 | 35 | AI147036 | AI147036 | q15b02.x |
| C | 32 | 44 | 9.1 | 420 | 21 | AA085410 | AA085410 | zn07903.s |
| C | 33 | 44 | 9.1 | 425 | 31 | AA847029 | AA847029 | oe09e01.s |
| C | 34 | 43 | 8.8 | 353 | 27 | AA507837 | AA507837 | ng86d05.s |
| C | 35 | 43 | 8.8 | 667 | 27 | AA186390 | AA186390 | zp99b10.s |
| C | 36 | 43 | 8.8 | 990 | 110 | AQ747348 | AQ747348 | HS_5536-B |
| C | 37 | 42 | 8.6 | 246 | 85 | F34489 | F34489 | HSPD29378.H |
| C | 38 | 42 | 8.6 | 395 | 27 | AA490097 | AA490097 | ea28h07.s |
| C | 39 | 42 | 8.6 | 413 | 106 | AO554565 | AO554565 | RPCI-1-B |
| C | 40 | 42 | 8.6 | 497 | 33 | AA933227 | AA933227 | ou02d08.s |
| C | 41 | 42 | 8.6 | 627 | 94 | AO114141 | AO114141 | CIT-HSP-2 |
| C | 42 | 42 | 8.6 | 629 | 107 | AO535928 | AO535928 | RPCI-11-B |
| C | 43 | 41 | 8.6 | 181 | 27 | AA471377 | AA471377 | PM11i49.K |
| C | 44 | 41 | 8.4 | 262 | 29 | AA622472 | AA622472 | nq07g09.s |
| C | 45 | 41 | 8.4 | 366 | 89 | TA1332 | TA1332 | ph1e6_19/1T |

| RESULT | 1 |
|------------|--|
| AA433099/c | |
| LOCUS | |
| DEFINITION | |
| AA433099 | 162 bp mRNA EST 13-AUG-1997 |
| g966d01.s1 | NCI-CGAP-Thy1 Homo sapiens cDNA clone IMAGE:542625 |
| | similar to contigens Alu repetitive element;contains element M59 |

| | | |
|-----------|--|---|
| ACCESSION | AA493099 | MER3 repetitive element ;, mRNA sequence. |
| VERSION | AA493099.1 | GI:2222940 |
| KEYWORDS | EST. | |
| SOURCE | human. | |
| ORGANISM | Homo sapiens | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | |
| AUTHORS | 1 (bases 1 to 162) | |
| TITLE | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . | |
| JOURNAL | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index | |
| COMMENT | Unpublished (1997) | |
| | On Jan 14, 1998 this sequence version replaced gi:11798572. | |

1. .162

CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arranged by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
www-bio.linn.gov/dbfp/image/image.html
Insert length: 451 Std Error: 0.00
Seq primer: -40ml3 fwd. Ex from Amersham
High quality sequence stop: 153.

47 a 36 c 50 g 2

| | | | | |
|---------------------------|---------|--------------------|--------|-------------------|
| Query Match | 24.5% | Score 119; | DB 27; | Length 162; |
| Best Local Similarity | 100.00; | Pred. No. 9.2e-46; | | |
| Matches 119; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0; |

274 tttagtacagacggggtcttcgcacacttggccaggtgtcttgaactcctgaactgtg 333

Db 162 TTTAGTACAGACGGGTTTCGCCACCTTGGCCAGGCTGGTCTTGAACCTCCTGACCTTGTG 103

Db 102 ATCAACCCACTCTAGTCTCTCCCAAGTCTGGGATTACAGGTGTGAGAGACCGCACCCAG 44

| RESULT | 2 |
|------------|--|
| LOCUS | W07101/c |
| DEFINITION | W07101 300 bp mRNA EST 25-APR-1996 Z89306.f1 Soares_fetal_lung_NbHL9w Homo sapiens cDNA clone IMAGE:300107 5' similar to contig16 Alu repetitive element; contains element MER22 repetitive element; mRNA sequence. |

| | |
|-----------|--------------|
| ACCESSION | W07101 |
| VERSION | W07101.1 |
| KEYWORDS | GI:128114 |
| SOURCE | EST. |
| ORGANISM | human. |
| | Homo sapiens |

REFERENCE
AUTHORS
1. Miller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Phases 1 to 300)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi